

SEQUENCE LISTING

<110> BACHMANN, Heinrich
BRUGGER, Roland
FRIEDLEIN, Arno M
WIRTZ, Gabriele M
WOGGON, Wolf-Dietrich
WYSS, Adrian
WYSS, Markus

<120> BETA,BETA-CAROTENE 15,15'-DIOXYGENASES, NUCLEIC ACID
SEQUENCES CODING THEREFOR AND THEIR USE

<130> B,B-CAROTENE 15,15'-DIOXYGENASES,...

<140>

<141>

<150> 103382.0

<151> 1999-02-22

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 526

<212> PRT

<213> CHICKEN

<400> 1

Met	Glu	Thr	Ile	Phe	Asn	Arg	Asn	Lys	Glu	Glu	His	Pro	Glu	Pro	Ile
1					5				10					15	

Lys	Ala	Glu	Val	Gln	Gly	Gln	Leu	Pro	Thr	Trp	Leu	Gln	Gly	Val	Leu
			20					25					30		

Leu	Arg	Asn	Gly	Pro	Gly	Met	His	Thr	Ile	Gly	Asp	Thr	Lys	Tyr	Asn
		35					40					45			

His	Trp	Phe	Asp	Gly	Leu	Ala	Leu	Leu	His	Ser	Phe	Thr	Phe	Lys	Asn
	50					55					60				

Gly	Glu	Val	Tyr	Tyr	Arg	Ser	Lys	Tyr	Leu	Arg	Ser	Asp	Thr	Tyr	Asn
65					70				75					80	

Cys	Asn	Ile	Glu	Ala	Asn	Arg	Ile	Val	Val	Ser	Glu	Phe	Gly	Thr	Met
				85				90						95	

Ala Tyr Pro Asp Pro Cys Lys Asn Ile Phe Ala Lys Ala Phe Ser Tyr
100 105 110

Leu Ser His Thr Ile Pro Glu Phe Thr Asp Asn Cys Leu Ile Asn Ile
115 120 125

Met Lys Thr Gly Asp Asp Tyr Tyr Ala Thr Ser Glu Thr Asn Phe Ile
130 135 140

Arg Lys Ile Asp Pro Gln Thr Leu Glu Thr Leu Asp Lys Val Asp Tyr
145 150 155 160

Ser Lys Tyr Val Ala Val Asn Leu Ala Thr Ser His Pro His Tyr Asp
165 170 175

Ser Ala Gly Asn Ile Leu Asn Met Gly Thr Ser Ile Val Asp Lys Gly
180 185 190

Arg Thr Lys Tyr Val Leu Phe Lys Ile Pro Ser Ser Val Pro Glu Lys
195 200 205

Glu Lys Lys Lys Ser Cys Phe Lys His Leu Glu Val Val Cys Ser Ile
210 215 220

Pro Ser Arg Ser Leu Leu Gln Pro Ser Tyr Tyr His Ser Phe Gly Ile
225 230 235 240

Thr Glu Asn Tyr Ile Val Phe Ile Glu Gln Pro Phe Lys Leu Asp Ile
245 250 255

Val Lys Leu Ala Thr Ala Tyr Ile Arg Gly Val Asn Trp Ala Ser Cys
260 265 270

Leu Ser Phe His Lys Glu Asp Lys Thr Trp Phe His Phe Val Asp Arg
275 280 285

Lys Thr Lys Lys Glu Val Ser Thr Lys Phe Tyr Thr Asp Ala Leu Val
290 295 300

Leu Tyr His His Ile Asn Ala Tyr Glu Glu Asp Gly His Val Val Phe
305 310 315 320

Asp Ile Val Ala Tyr Arg Asp Asn Ser Leu Tyr Asp Met Phe Tyr Leu
325 330 335

Lys Lys Leu Asp Lys Asp Phe Glu Val Asn Asn Lys Leu Thr Ser Ile
340 345 350

Pro Thr Cys Lys Arg Phe Val Val Pro Leu Gln Tyr Asp Lys Asp Ala
 355 360 365

Glu Val Gly Ser Asn Leu Val Lys Leu Pro Thr Ser Ala Thr Ala Val
 370 375 380

Lys Glu Lys Asp Gly Ser Ile Tyr Cys Gln Pro Glu Ile Leu Cys Glu
 385 390 395 400

Gly Ile Glu Leu Pro Arg Val Asn Tyr Asp Tyr Asn Gly Lys Lys Tyr
 405 410 415

Lys Tyr Val Tyr Ala Thr Glu Val Gln Trp Ser Pro Val Pro Thr Lys
 420 425 430

Ile Ala Lys Leu Asn Val Gln Thr Lys Glu Val Leu His Trp Gly Glu
 435 440 445

Asp His Cys Trp Pro Ser Glu Pro Ile Phe Val Pro Ser Pro Asp Ala
 450 455 460

Arg Glu Glu Asp Glu Gly Val Val Leu Thr Cys Val Val Val Ser Glu
 465 470 475 480

Pro Asn Lys Ala Pro Phe Leu Leu Ile Leu Asp Ala Lys Thr Phe Lys
 485 490 495

Glu Leu Gly Arg Ala Thr Val Asn Val Glu Met His Leu Asp Leu His
 500 505 510

Gly Met Phe Ile Pro Gln Asn Asp Leu Gly Ala Glu Thr Glu
 515 520 525

<210> 2

<211> 3111

<212> DNA

<213> CHICKEN

<400> 2

cggatccact agtaacggcc gccagtgtgg tggaatccat ccttctatgt aacaggaaag 60
 agctgttctt agcccagaga ggagggcacc gtacgcctgc aggagcagct gggtagagga 120
 cacaggagag cgatggagac aatatttaac agaaacaaag aagagcatcc agagcccata 180
 aaagctgagg tgcaaggtca gttgccact tgggtgcaag gggacttct cggaaatggc 240
 ccagggatgc acacaatagg ggacactaaa tacaaccact ggtttgatgg cttggctctg 300
 ctgcacagct tcacgtttaa aaatggtgaa gtttactaca gaagtaagta cctccgaagt 360
 gacacataca actgcaatat agaagcaaac cgaatcgtgg tgtctgagtt tggaaccatg 420

gcttatccgg atccatgcaa aaacatattt gccaaaggcat tctcatactt atctcacacc 480
attcctgagt tcacggacaa ctgcctgata aacattatga aaactgggga tgattattat 540
gctaccagtg agactaactt catcagaaaa attgatccac agactctgga gacactagat 600
aaggtagact acagcaaata tgtagctgta aacttggcaa cttctcacc acactatgac 660
agtgcctggaa atattctcaa catgggtact tcaattgttg ataaaggagg aacaaaatat 720
gttctcttta agatcccttc ctctgtacca gaaaaagaaa agaagaaatc ttgttttaaa 780
cacctggaag tagtatgttc catcccttct cgctccctgc tccaaccaag ctactaccac 840
agctttggaa tcacagaaaa ttatatgttg ttcatagagc agccatttaa actggatatt 900
gtcaaaactgg caactgccta catccgaggt gtgaactggg cttcctgcct ttcctttcat 960
aaggaggata agacgtgggt tcactttgta gacagaaaaga cgaaaaaaga agtatccacc 1020
aagttttaca ctgatgcttt ggtgctttat caccacataa atgcttacga agaagatggc 1080
cacgttggtt ttgatatcgt tgcctacaga gacaatagct tgtacgatat gttttactta 1140
aaaaaactgg acaaagactt tgaagtgaac aacaagctta cctccatccc aacctgcaag 1200
cgctttgttg tgcctctgca gtatgacaag gatgcagaag taggttctaa tttagtcaaa 1260
cttccaactt ccgcaactgc tgtaaaagaa aaagatggca gcatctattg tcaacctgaa 1320
atattatgtg aagggataga actgcctcgt gtcaactatg actacaatgg caaaaaatac 1380
aagtatgtct atgcaacaga agtccagtgg agcccagttc ctacaaagat tgcaaaactg 1440
aatgtccaaa caaaggaagt actgactgg ggagaagacc actgctggcc ctgagagccc 1500
atctttgttc ccagccccga tgcaagagaa gaggatgaag gtgttggttt gacctgtgtt 1560
gtggtgtctg agccaaataa agcacccttc ctactcatct tggatgctaa aacattcaaa 1620
gaattggggc gagccacagt taacgtagaa atgcatctgg acctgcatgg gatgtttata 1680
ccacagaatg atttgggggc tgagacggaa taaaacgcta ttgatccgac tacacaaact 1740
gagacaactt tctactgaac atgagttaat atccctttta ccattcaaga acaaccatat 1800
aacgacacaa aatgactatg tataatctct taaataatag atataatcct ttttaaggcac 1860
agcgatgagt ttactacag gtaacgatat gcacaactgg catataacta ttccaaaaga 1920
agaagaacga tcagtgtttt agaagtgcta atgttgtaaca taacggcggc agagggaaca 1980
ggagagaaag gtaacgggaa tatttaatat aatatagatt tctgagcaaa tgaagtgcag 2040
tatttatggt gtgatgcag gcgatgagca cataggtctg cagctcatgt atcttttaga 2100
gatcgtttca agattgcagc ttgtgatgca agttttctcc agccagaaaa cctcatttta 2160
aaccatctgc tactggtaat tcataccaat gcattttctt ggtgctcgat ttacactata 2220
accaaagtta agtattacat tcaggtgcta caactttcta atttacaacc gaaacaaaca 2280
agcaaacagc acttgctttg ctaataaccc catggtgtat ttttcctttt tatgatgaca 2340
aaaccaagta catatgggtt tatgtagcat tcaattatac ttcagtgcta ttccatccta 2400
atgttataag caatttgat ttaaatacgt tttccttgag aatatctgac ataacatttt 2460
gtgtaatgag atgactatgt tgtctaaaga tgaacaggaa tgtatctttt attagtattg 2520
ttaattgtgt tactaatact atgcatatga atgagagcaa tgtatttcta ggagaactca 2580
gatatacatt caacaatttc tgtaggtgaa aatgcattta ctgatgaaag ttgaatcgtt 2640
aatgagggag aaaactgggt atccatccat ccaactatgt taggtgttca cctgggtctgt 2700
atgtgacacc acgctgtttg ggtatctctc actttcacat acctgttctc atgggtttctg 2760
ctactcactg tttttgag gagagaaaca aaatgaaatc actgtcactt actatcgccc 2820
catcacataa gaacaatggg gctttggtga cttgttcatg attacataag atgtttgcag 2880
cagagcagca atagaacca caccatccac agttcttgct tgctctgta tgactccctt 2940
tgctgtcttt atggtttgca tgtatgaaga atacactgcc taattctaata gttaaaaagt 3000
cactggggtc agatctagag cttaagtaag cagtctgggg ttttcaaagt tttatatgtt 3060
ccataaaatg gaaataaaca cctccataat aaaaaaaaaa aaaaaaaaaa a 3111

<210> 3

<211> 8
<212> PRT
<213> CHICKEN

<400> 3
Ala Glu Val Gln Gly Gln Leu Pro
1 5

<210> 4
<211> 506
<212> PRT
<213> CHICKEN

<400> 4
Glu Glu His Pro Glu Pro Ile Lys Ala Glu Val Gln Gly Gln Leu Pro
1 5 10 15

Thr Trp Leu Gln Gly Val Leu Leu Arg Asn Gly Pro Gly Met His Thr
20 25 30

Ile Gly Asp Thr Lys Tyr Asn His Trp Phe Asp Gly Leu Ala Leu Leu
35 40 45

His Ser Phe Thr Phe Lys Asn Gly Glu Val Tyr Tyr Arg Ser Lys Tyr
50 55 60

Leu Arg Ser Asp Thr Tyr Asn Cys Asn Ile Glu Ala Asn Arg Ile Val
65 70 75 80

Val Ser Glu Phe Gly Thr Met Ala Tyr Pro Asp Pro Cys Lys Asn Ile
85 90 95

Phe Ala Lys Ala Phe Ser Tyr Leu Ser His Thr Ile Pro Glu Phe Thr
100 105 110

Asp Asn Cys Leu Ile Asn Ile Met Lys Thr Gly Asp Asp Tyr Tyr Ala
115 120 125

Thr Ser Glu Thr Asn Phe Ile Arg Lys Ile Asp Pro Gln Thr Leu Glu
130 135 140

Thr Leu Asp Lys Val Asp Tyr Ser Lys Tyr Val Ala Val Asn Leu Ala
145 150 155 160

Thr Ser His Pro His Tyr Asp Ser Ala Gly Asn Ile Leu Asn Met Gly
165 170 175

Thr	Ser	Ile	Val	Asp	Lys	Gly	Arg	Thr	Lys	Tyr	Val	Leu	Phe	Lys	Ile	180	185	190
Pro	Ser	Ser	Val	Pro	Glu	Lys	Glu	Lys	Lys	Lys	Ser	Cys	Phe	Lys	His	195	200	205
Leu	Glu	Val	Val	Cys	Ser	Ile	Pro	Ser	Arg	Ser	Leu	Leu	Gln	Pro	Ser	210	215	220
Tyr	Tyr	His	Ser	Phe	Gly	Ile	Thr	Glu	Asn	Tyr	Ile	Val	Phe	Ile	Glu	225	230	235 240
Gln	Pro	Phe	Lys	Leu	Asp	Ile	Val	Lys	Leu	Ala	Thr	Ala	Tyr	Ile	Arg	245	250	255
Gly	Val	Asn	Trp	Ala	Ser	Cys	Leu	Ser	Phe	His	Lys	Glu	Asp	Lys	Thr	260	265	270
Trp	Phe	His	Phe	Val	Asp	Arg	Lys	Thr	Lys	Lys	Glu	Val	Ser	Thr	Lys	275	280	285
Phe	Tyr	Thr	Asp	Ala	Leu	Val	Leu	Tyr	His	His	Ile	Asn	Ala	Tyr	Glu	290	295	300
Glu	Asp	Gly	His	Val	Val	Phe	Asp	Ile	Val	Ala	Tyr	Arg	Asp	Asn	Ser	305	310	315 320
Leu	Tyr	Asp	Met	Phe	Tyr	Leu	Lys	Lys	Leu	Asp	Lys	Asp	Phe	Glu	Val	325	330	335
Asn	Asn	Lys	Leu	Thr	Ser	Ile	Pro	Thr	Cys	Lys	Arg	Phe	Val	Val	Pro	340	345	350
Leu	Gln	Tyr	Asp	Lys	Asp	Ala	Glu	Val	Gly	Ser	Asn	Leu	Val	Lys	Leu	355	360	365
Pro	Thr	Ser	Ala	Thr	Ala	Val	Lys	Glu	Lys	Asp	Gly	Ser	Ile	Tyr	Cys	370	375	380
Gln	Pro	Glu	Ile	Leu	Cys	Glu	Gly	Ile	Glu	Leu	Pro	Arg	Val	Asn	Tyr	385	390	395 400
Asp	Tyr	Asn	Gly	Lys	Lys	Tyr	Lys	Tyr	Val	Tyr	Ala	Thr	Glu	Val	Gln	405	410	415
Trp	Ser	Pro	Val	Pro	Thr	Lys	Ile	Ala	Lys	Leu	Asn	Val	Gln	Thr	Lys	420	425	430

Glu Val Leu His Trp Gly Glu Asp His Cys Trp Pro Ser Glu Pro Ile
 435 440 445

Phe Val Pro Ser Pro Asp Ala Arg Glu Glu Asp Glu Gly Val Val Leu
 450 455 460

Thr Cys Val Val Val Ser Glu Pro Asn Lys Ala Pro Phe Leu Leu Ile
 465 470 475 480

Leu Asp Ala Lys Thr Phe Lys Glu Leu Gly Arg Ala Thr Val Asn Val
 485 490 495

Glu Met His Leu Asp Leu His Gly Met Phe
 500 505

<210> 5

<211> 529

<212> PRT

<213> BOVINE

<400> 5

Glu Glu Leu Ser Ser Pro Leu Thr Ala His Val Thr Gly Arg Ile Pro
 1 5 10 15

Leu Trp Leu Thr Gly Ser Leu Leu Arg Cys Phe Thr Gly Pro Gly Leu
 20 25 30

Phe Glu Val Gly Ser Glu Pro Phe Tyr His Leu Phe Asp Gly Gln Ala
 35 40 45

Leu Leu His Lys Phe Asp Phe Lys Glu Gly His Val Thr Tyr His Arg
 50 55 60

Arg Phe Ile Arg Thr Asp Ala Tyr Val Arg Ala Met Thr Glu Lys Arg
 65 70 75 80

Ile Val Ile Thr Glu Phe Gly Phe Thr Thr Cys Ala Phe Pro Asp Pro
 85 90 95

Cys Lys Asn Ile Phe Ser Arg Phe Phe Ser Tyr Phe Arg Gly Val Glu
 100 105 110

Val Thr Asp Asn Ala Leu Val Asn Val Tyr Pro Val Gly Glu Asp Tyr
 115 120 125

Tyr Ala Cys Thr Glu Thr Asn Phe Ile Thr Lys Ile Asn Pro Glu Thr
 130 135 140

Leu Glu Thr Ile Phe Thr Lys Gln Val Asp Leu Cys Asn Tyr Val Ser
 145 150 155 160
 Val Asn Gly Ala Thr Ala His Pro His Ile Glu Asn Asp Gly Thr Val
 165 170 175
 Tyr Asn Ile Gly Asn Cys Phe Gly Lys Asn Phe Ser Ile Ala Tyr Asn
 180 185 190
 Ile Val Lys Ile Pro Pro Leu Gln Ala Asp Lys Glu Asp Pro Ile Ser
 195 200 205
 Lys Phe Thr Ser Glu Ile Val Val Gln Phe Pro Cys Ser Asp Arg Phe
 210 215 220
 Lys Pro Ser Tyr Val His Ser Phe Gly Leu Thr Pro Asn Tyr Ile Val
 225 230 235 240
 Phe Val Glu Thr Pro Val Lys Ile Asn Leu Phe Lys Phe Leu Ser Ser
 245 250 255
 Trp Ser Leu Trp Gly Ala Asn Tyr Met Asp Cys Phe Glu Ser Phe Thr
 260 265 270
 Asn Glu Thr Met Gly Val Trp Leu His Ile Ala Asp Lys Lys Arg Lys
 275 280 285
 Lys Tyr Leu Asn Asn Lys Tyr Arg Thr Ser Pro Phe Asn Leu Phe His
 290 295 300
 His Ile Asn Thr Tyr Glu Asp Asn Gly Phe Leu Ile Val Asp Leu Cys
 305 310 315 320
 Cys Trp Lys Gly Phe Glu Phe Val Tyr Asn Tyr Phe Thr Leu Tyr Leu
 325 330 335
 Ala Asn Leu Arg Glu Asn Trp Glu Glu Val Lys Lys Asn Ala Arg Lys
 340 345 350
 Ala Pro Gln Pro Glu Val Arg Arg Tyr Val Leu Pro Leu Asn Ile Asp
 355 360 365
 Lys Ala Asp Thr Gly Lys Asn Leu Val Thr Leu Pro Asn Thr Thr Ala
 370 375 380
 Thr Ala Ile Leu Cys Ser Asp Glu Phe Thr Thr Ile Trp Leu Glu Pro
 385 390 395 400

Glu Val Leu Phe Ser Gly Pro Arg Gln Ala Phe Glu Phe Pro Gln Ile
 405 410 415

Asn Tyr Gln Lys Tyr Cys Gly Lys Pro Tyr Thr Tyr Ala Tyr Gly Leu
 420 425 430

Gly Leu Asn His Phe Val Pro Asp Arg Leu Cys Lys Leu Asn Val Lys
 435 440 445

Thr Lys Glu Thr Trp Phe Thr Val Trp Gln Glu Pro Asp Ser Tyr Pro
 450 455 460

Ser Glu Pro Ile Phe Val Ser His Pro Asp Ala Leu Glu Glu Asp Asp
 465 470 475 480

Gly Val Val Leu Ser Val Val Val Ser Pro Gly Ala Gly Gln Lys Pro
 485 490 495

Ala Tyr Leu Leu Ile Leu Asn Ala Lys Asp Leu Ser Glu Val Ala Arg
 500 505 510

Ala Glu Phe Thr Val Glu Ile Asn Ile Pro Val Thr Phe His Gly Leu
 515 520 525

Phe

<210> 6
 <211> 18
 <212> PRT
 <213> CHICKEN

<400> 6
 Asn Lys Glu Glu His Pro Glu Pro Ile Lys Ala Glu Val Gln Gly Gln
 1 5 10 15

Leu Pro

<210> 7
 <211> 18
 <212> PRT
 <213> CHICKEN

<400> 7

Asn Lys Glu Glu His Pro Glu Pro Ile Lys Ala Glu Val Gln Gly Gln
1 5 10 15

Leu Pro

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<220>

<221> modified_base

<222> (18)

<223> i

<400> 8

aacaargarg ascayccnga

20

<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<220>

<221> modified_base

<222> (7)

<223> i

<220>

<221> modified_base

<222> (13)

<223> i

<400> 9

sagctgnccc tgnacytcsg c

21

<210> 10

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

tctgaattcc ggagcccata aaagc

25